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MPSRCH (TM)

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Release 2.1D John F. Collins, Biocomputing Research Unit.  
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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Jan 21 19:36:37 1997; MasPar time 113.81 Seconds  
899.019 Million cell updates/sec

Tabular output not generated.

Title: >US-08-469-637-1  
Description: (1-1173) from US08469637.seq  
Perfect Score: 1173  
N.A. Sequence: 1 ATGAACAAGTTGCTGTGCTG.....TTTTTAGAAATGATAGGTAA 1173  
Comp: TACTTGTTCAACGACACGAC.....AAAAATCTTTACTATCCATT

Scoring table: TABLE default  
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 113505 seqs, 43611913 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: n-geneseq25  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22

Statistics: Mean 9.225; Variance 5.200; scale 1.774

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	%	Query					
No.	Score	Match Length	DB	ID	Description	Pred. No.	

	1	85	7.2	1047	2	Q10572	Human Natriuretic Pep	6.75e-40
c	2	63	5.4	1047	2	Q10572	Human Natriuretic Pep	6.29e-25
	3	45	3.8	91	9	Q51746	Oligonucleotide probe	2.82e-13
	4	42	3.6	204	1	N81164	Base substituted E.co	2.03e-11
c	5	39	3.3	91	9	Q51746	Oligonucleotide probe	1.36e-09
c	6	37	3.2	204	1	N81164	Base substituted E.co	2.14e-08
	7	36	3.1	114	12	Q70465	Generic DNA sequence	8.34e-08
	8	36	3.1	114	12	Q70469	Generic DNA sequence	8.34e-08
	9	36	3.1	114	12	Q70470	Generic DNA sequence	8.34e-08
	10	35	3.0	114	12	Q70467	Generic DNA sequence	3.22e-07
c	11	34	2.9	114	12	Q70467	Generic DNA sequence	1.23e-06
	12	33	2.8	114	12	Q70468	Generic DNA sequence	4.61e-06
	13	33	2.8	114	12	Q70466	Generic DNA sequence	4.61e-06
c	14	33	2.8	114	12	Q70468	Generic DNA sequence	4.61e-06
	15	32	2.7	114	12	Q70473	Generic DNA sequence	1.71e-05
c	16	32	2.7	114	12	Q70465	Generic DNA sequence	1.71e-05
c	17	32	2.7	114	12	Q70469	Generic DNA sequence	1.71e-05
	18	31	2.6	114	12	Q70472	Generic DNA sequence	6.27e-05
	19	30	2.6	114	12	Q70471	Generic DNA sequence	2.26e-04
c	20	30	2.6	114	12	Q70470	Generic DNA sequence	2.26e-04
c	21	30	2.6	114	12	Q70466	Generic DNA sequence	2.26e-04
c	22	28	2.4	114	12	Q70472	Generic DNA sequence	2.80e-03
c	23	28	2.4	114	12	Q70473	Generic DNA sequence	2.80e-03
c	24	27	2.3	114	12	Q70471	Generic DNA sequence	9.57e-03
	25	26	2.2	81	21	T13611	DC43 TSAR library gen	3.21e-02
	26	25	2.1	74	21	T13613	DC43 TSAR library gen	1.06e-01
	27	25	2.1	565	6	Q35072	HCV envelope region n	1.06e-01
	28	23	2.0	82	21	T13610	DC43 TSAR library gen	1.06e+00
c	29	23	2.0	82	21	T13610	DC43 TSAR library gen	1.06e+00
c	30	23	2.0	146	21	T13624	ME#2b library generat	1.06e+00
	31	24	2.0	498	3	N50034	Sequence encoding new	3.39e-01
	32	24	2.0	501	3	N50025	Sequence encoding new	3.39e-01
	33	24	2.0	501	3	N50031	Sequence encoding new	3.39e-01
	34	24	2.0	501	3	N50028	Sequence encoding new	3.39e-01
	35	24	2.0	501	3	N50032	Sequence encoding new	3.39e-01
c	36	23	2.0	3871	2	N71302	HSV-1 gB and surround	1.06e+00
c	37	22	1.9	66	21	T13585	TSAR-9 library genera	3.25e+00
c	38	22	1.9	69	21	T13583	TSAR-9 library genera	3.25e+00
	39	22	1.9	75	21	T13612	DC43 TSAR library gen	3.25e+00
c	40	22	1.9	75	21	T13612	DC43 TSAR library gen	3.25e+00
c	41	22	1.9	469	20	T29603	Human EHOC-1 exon 7 r	3.25e+00
	42	22	1.9	501	3	N50027	Sequence encoding new	3.25e+00
	43	22	1.9	501	3	N50029	Sequence encoding new	3.25e+00
	44	22	1.9	2492	1	N93099	FUS2 Gene.	3.25e+00
	45	22	1.9	3812	2	Q10991	Partial sequence of m	3.25e+00